

RAW SEQUENCE LISTING

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Application Serial Number: 09/747, 521B
Source: IFW16
Date Processed by STIC: 11/20/2006

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IFW16

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DATE: 11/20/2006

PATENT APPLICATION: US/09/747,521B

TIME: 13:38:16

Input Set : N:\efs\09747521b_efs\sequen1.txt

Output Set: N:\CRF4\11202006\I747521B.raw

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3 <110> APPLICANT: GALLOWAY, DARREL R.
4   MATECZUN, ALFRED J.
6 <120> TITLE OF INVENTION: METHODS FOR PROTECTION AGAINST LETHAL INFECTION WITH
7   BACILLUS ANTHRACIS
9 <130> FILE REFERENCE: 22727-04079
11 <140> CURRENT APPLICATION NUMBER: 09/747,521B
12 <141> CURRENT FILING DATE: 2000-12-21
14 <150> PRIOR APPLICATION NUMBER: 60/171,459
15 <151> PRIOR FILING DATE: 1999-12-22
17 <160> NUMBER OF SEQ ID NOS: 10
19 <170> SOFTWARE: PatentIn Ver. 3.3
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2430
23 <212> TYPE: DNA
24 <213> ORGANISM: Bacillus anthracis
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)..(2427)
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33   1               5               10               15
35 gta aca gca att act ttg agt ggt ccc gtc ttt atc ccc ctt gta cag      96
36 Val Thr Ala Ile Thr Leu Ser Gly Pro Val Phe Ile Pro Leu Val Gln
37   20               25               30
39 ggg gcg ggc ggt cat ggt gat gta ggt atg cac gta aaa gag aaa gag      144
40 Gly Ala Gly Gly His Gly Asp Val Gly Met His Val Lys Glu Lys Glu
41   35               40               45
43 aaa aat aaa gat gag aat aag aga aaa gat gaa gaa cga aat aaa aca      192
44 Lys Asn Lys Asp Glu Asn Lys Arg Lys Asp Glu Glu Arg Asn Lys Thr
45   50               55               60
47 cag gaa gag cat tta aag gaa atc atg aaa cac att gta aaa ata gaa      240
48 Gln Glu Glu His Leu Lys Glu Ile Met Lys His Ile Val Lys Ile Glu
49   65               70               75               80
51 gta aaa ggg gag gaa gct gtt aaa aaa gag gca gca gaa aag cta ctt      288
52 Val Lys Gly Glu Glu Ala Val Lys Lys Glu Ala Ala Glu Lys Leu Leu
53   85               90               95
55 gag aaa gta cca tct gat gtt tta gag atg tat aaa gca att gga gga      336
56 Glu Lys Val Pro Ser Asp Val Leu Glu Met Tyr Lys Ala Ile Gly Gly
57   100              105              110
59 aag ata tat att gtg gat ggt gat att aca aaa cat ata tct tta gaa      384
60 Lys Ile Tyr Ile Val Asp Gly Asp Ile Thr Lys His Ile Ser Leu Glu
61   115              120              125

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63 gca tta tct gaa gat aag aaa aaa ata aaa gac att tat ggg aaa gat 432
64 Ala Leu Ser Glu Asp Lys Lys Lys Ile Lys Asp Ile Tyr Gly Lys Asp
65 130 135 140
67 gct tta tta cat gaa cat tat gta tat gca aaa gaa gga tat gaa ccc 480
68 Ala Leu Leu His Glu Tyr Val Tyr Ala Lys Glu Gly Tyr Glu Pro
69 145 150 155 160
71 gta ctt gta atc caa tct tcg gaa gat tat gta gaa aat act gaa aag 528
72 Val Leu Val Ile Gln Ser Ser Glu Asp Tyr Val Glu Asn Thr Glu Lys
73 165 170 175
75 gca ctg aac gtt tat tat gaa ata ggt aag ata tta tca agg gat att 576
76 Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys Ile Leu Ser Arg Asp Ile
77 180 185 190
79 tta agt aaa att aat caa cca tat cag aaa ttt tta gat gta tta aat 624
80 Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys Phe Leu Asp Val Leu Asn
81 195 200 205
83 acc att aaa aat gca tct gat tca gat gga caa gat ctt tta ttt act 672
84 Thr Ile Lys Asn Ala Ser Asp Ser Asp Gly Gln Asp Leu Leu Phe Thr
85 210 215 220
87 aat cag ctt aag gaa gat ccc aca gac ttt tct gta gaa ttc ttg gaa 720
88 Asn Gln Leu Lys Glu His Pro Thr Asp Phe Ser Val Glu Phe Leu Glu
89 225 230 235 240
91 caa aat agc aat gag gta caa gaa gta ttt gcg aaa gct ttt gca tat 768
92 Gln Asn Ser Asn Glu Val Gln Glu Val Phe Ala Lys Ala Phe Ala Tyr
93 245 250 255
95 tat atc gag cca cag cat cgt gat gtt tta cag ctt tat gca ccg gaa 816
96 Tyr Ile Glu Pro Gln His Arg Asp Val Leu Gln Leu Tyr Ala Pro Glu
97 260 265 270
99 gct ttt aat tac atg gat aaa ttt aac gaa caa gaa ata aat cta tcc 864
100 Ala Phe Asn Tyr Met Asp Lys Phe Asn Glu Gln Glu Ile Asn Leu Ser
101 275 280 285
103 ttg gaa gaa ctt aaa gat caa cgg atg ctg tca aga tat gaa aaa tgg 912
104 Leu Glu Glu Leu Lys Asp Gln Arg Met Leu Ser Arg Tyr Glu Lys Trp
105 290 295 300
107 gaa aag ata aaa cag cac tat caa cac tgg agc gat tct tta tct gaa 960
108 Glu Lys Ile Lys Gln His Tyr Gln His Trp Ser Asp Ser Leu Ser Glu
109 305 310 315 320
111 gaa gga aga gga ctt tta aaa aag ctg cag att cct att gag cca aag 1008
112 Glu Gly Arg Gly Leu Leu Lys Lys Leu Gln Ile Pro Ile Glu Pro Lys
113 325 330 335
115 aaa gat gac ata att cat tct tta tct caa gaa gaa aaa gag ctt cta 1056
116 Lys Asp Asp Ile Ile His Ser Leu Ser Gln Glu Glu Lys Glu Leu Leu
117 340 345 350
119 aaa aga ata caa att gat agt agt gat ttt tta tct act gag gaa aaa 1104
120 Lys Arg Ile Gln Ile Asp Ser Ser Asp Phe Leu Ser Thr Glu Glu Lys
121 355 360 365
123 gag ttt tta aaa aag cta caa att gat att cgt gat tct tta tct gaa 1152
124 Glu Phe Leu Lys Lys Leu Gln Ile Asp Ile Arg Asp Ser Leu Ser Glu
125 370 375 380
127 gaa gaa aaa gag ctt tta aat aga ata cag gtg gat agt agt aat cct 1200

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131 tta tct gaa aaa gaa aaa gag ttt tta aaa aag ctg aaa ctt gat att 1248
132 Leu Ser Glu Lys Glu Lys Glu Phe Leu Lys Lys Leu Lys Leu Asp Ile
133          405          410          415
135 caa cca tat gat att aat caa agg ttg caa gat aca gga ggg tta att 1296
136 Gln Pro Tyr Asp Ile Asn Gln Arg Leu Gln Asp Thr Gly Gly Leu Ile
137          420          425          430
139 gat agt ccg tca att aat ctt gat gta aga aag cag tat aaa agg gat 1344
140 Asp Ser Pro Ser Ile Asn Leu Asp Val Arg Lys Gln Tyr Lys Arg Asp
141          435          440          445
143 att caa aat att gat gct tta tta cat caa tcc att gga agt acc ttg 1392
144 Ile Gln Asn Ile Asp Ala Leu Leu His Gln Ser Ile Gly Ser Thr Leu
145          450          455          460
147 tac aat aaa att tat ttg tat gaa aat atg aat atc aat aac ctt aca 1440
148 Tyr Asn Lys Ile Tyr Leu Tyr Glu Asn Met Asn Ile Asn Asn Leu Thr
149 465          470          475          480
151 gca acc cta ggt gcg gat tta gtt gat tcc act gat aat act aaa att 1488
152 Ala Thr Leu Gly Ala Asp Leu Val Asp Ser Thr Asp Asn Thr Lys Ile
153          485          490          495
155 aat aga ggt att ttc aat gaa ttc aaa aaa aat ttc aaa tat agt att 1536
156 Asn Arg Gly Ile Phe Asn Glu Phe Lys Lys Asn Phe Lys Tyr Ser Ile
157          500          505          510
159 tct agt aac tat atg att gtt gat ata aat gaa agg cct gca tta gat 1584
160 Ser Ser Asn Tyr Met Ile Val Asp Ile Asn Glu Arg Pro Ala Leu Asp
161          515          520          525
163 aat gag cgt ttg aaa tgg aga atc caa tta tca cca gat act cga gca 1632
164 Asn Glu Arg Leu Lys Trp Arg Ile Gln Leu Ser Pro Asp Thr Arg Ala
165          530          535          540
167 gga tat tta gaa aat gga aag ctt ata tta caa aga aac atc ggt ctg 1680
168 Gly Tyr Leu Glu Asn Gly Lys Leu Ile Leu Gln Arg Asn Ile Gly Leu
169 545          550          555          560
171 gaa ata aag gat gta caa ata att aag caa tcc gaa aaa gaa tat ata 1728
172 Glu Ile Lys Asp Val Gln Ile Ile Lys Gln Ser Glu Lys Glu Tyr Ile
173          565          570          575
175 agg att gat gcg aaa gta gtg cca aag agt aaa ata gat aca aaa att 1776
176 Arg Ile Asp Ala Lys Val Val Pro Lys Ser Lys Ile Asp Thr Lys Ile
177          580          585          590
179 caa gaa gca cag tta aat ata aat cag gaa tgg aat aaa gca tta ggg 1824
180 Gln Glu Ala Gln Leu Asn Ile Asn Gln Glu Trp Asn Lys Ala Leu Gly
181          595          600          605
183 tta cca aaa tat aca aag ctt att aca ttc aac gtg cat aat aga tat 1872
184 Leu Pro Lys Tyr Thr Lys Leu Ile Thr Phe Asn Val His Asn Arg Tyr
185          610          615          620
187 gca tcc aat att gta gaa agt gct tat tta ata ttg aat gaa tgg aaa 1920
188 Ala Ser Asn Ile Val Glu Ser Ala Tyr Leu Ile Leu Asn Glu Trp Lys
189 625          630          635          640
191 aat aat att caa agt gat ctt ata aaa aag gta aca aat tac tta gtt 1968
192 Asn Asn Ile Gln Ser Asp Leu Ile Lys Lys Val Thr Asn Tyr Leu Val

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193          645          650          655
195 gat ggt aat gga aga ttt gtt ttt acc gat att act ctc cct aat ata 2016
196 Asp Gly Asn Gly Arg Phe Val Phe Thr Asp Ile Thr Leu Pro Asn Ile
197          660          665          670
199 gct gaa caa tat aca cat caa gat gag ata tat gag caa gtt cat tca 2064
200 Ala Glu Gln Tyr Thr His Gln Asp Glu Ile Tyr Glu Gln Val His Ser
201          675          680          685
203 aaa ggg tta tat gtt cca gaa tcc cgt tct ata tta ctc cat gga cct 2112
204 Lys Gly Leu Tyr Val Pro Glu Ser Arg Ser Ile Leu Leu His Gly Pro
205          690          695          700
207 tca aaa ggt gta gaa tta agg aat gat agt gag ggt ttt ata cac gaa 2160
208 Ser Lys Gly Val Glu Leu Arg Asn Asp Ser Glu Gly Phe Ile His Glu
209 705          710          715          720
211 ttt gga cat gct gtg gat gat tat gct gga tat cta tta gat aag aac 2208
212 Phe Gly His Ala Val Asp Asp Tyr Ala Gly Tyr Leu Leu Asp Lys Asn
213          725          730          735
215 caa tct gat tta gtt aca aat tct aaa aaa ttc att gat att ttt aag 2256
216 Gln Ser Asp Leu Val Thr Asn Ser Lys Lys Phe Ile Asp Ile Phe Lys
217          740          745          750
219 gaa gaa ggg agt aat tta act tcg tat ggg aga aca aat gaa gcg gaa 2304
220 Glu Glu Gly Ser Asn Leu Thr Ser Tyr Gly Arg Thr Asn Glu Ala Glu
221          755          760          765
223 ttt ttt gca gaa gcc ttt agg tta atg cat tct acg gac cat gct gaa 2352
224 Phe Phe Ala Glu Ala Phe Arg Leu Met His Ser Thr Asp His Ala Glu
225          770          775          780
227 cgt tta aaa gtt caa aaa aat gct ccg aaa act ttc caa ttt att aac 2400
228 Arg Leu Lys Val Gln Lys Asn Ala Pro Lys Thr Phe Gln Phe Ile Asn
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238 <212> TYPE: PRT
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248 Gly Ala Gly Gly His Gly Asp Val Gly Met His Val Lys Glu Lys Glu
249 35 40 45
251 Lys Asn Lys Asp Glu Asn Lys Arg Lys Asp Glu Glu Arg Asn Lys Thr
252 50 55 60
254 Gln Glu Glu His Leu Lys Glu Ile Met Lys His Ile Val Lys Ile Glu
255 65 70 75 80
257 Val Lys Gly Glu Glu Ala Val Lys Lys Glu Ala Ala Glu Lys Leu Leu
258 85 90 95
260 Glu Lys Val Pro Ser Asp Val Leu Glu Met Tyr Lys Ala Ile Gly Gly

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261          100          105          110
263 Lys Ile Tyr Ile Val Asp Gly Asp Ile Thr Lys His Ile Ser Leu Glu
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266 Ala Leu Ser Glu Asp Lys Lys Lys Ile Lys Asp Ile Tyr Gly Lys Asp
267          130          135          140
269 Ala Leu Leu His Glu His Tyr Val Tyr Ala Lys Glu Gly Tyr Glu Pro
270 145          150          155          160
272 Val Leu Val Ile Gln Ser Ser Glu Asp Tyr Val Glu Asn Thr Glu Lys
273          165          170          175
275 Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys Ile Leu Ser Arg Asp Ile
276          180          185          190
278 Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys Phe Leu Asp Val Leu Asn
279          195          200          205
281 Thr Ile Lys Asn Ala Ser Asp Ser Asp Gly Gln Asp Leu Leu Phe Thr
282          210          215          220
284 Asn Gln Leu Lys Glu His Pro Thr Asp Phe Ser Val Glu Phe Leu Glu
285 225          230          235          240
287 Gln Asn Ser Asn Glu Val Gln Glu Val Phe Ala Lys Ala Phe Ala Tyr
288          245          250          255
290 Tyr Ile Glu Pro Gln His Arg Asp Val Leu Gln Leu Tyr Ala Pro Glu
291          260          265          270
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294          275          280          285
296 Leu Glu Glu Leu Lys Asp Gln Arg Met Leu Ser Arg Tyr Glu Lys Trp
297          290          295          300
299 Glu Lys Lys Ile Lys Gln His Tyr Gln His Trp Ser Asp Ser Leu Ser Glu
300 305          310          315          320
302 Glu Gly Arg Gly Leu Leu Lys Lys Leu Gln Ile Pro Ile Glu Pro Lys
303          325          330          335
305 Lys Asp Asp Ile Ile His Ser Leu Ser Gln Glu Glu Lys Glu Leu Leu
306          340          345          350
308 Lys Arg Ile Gln Ile Asp Ser Ser Asp Phe Leu Ser Thr Glu Glu Lys
309          355          360          365
311 Glu Phe Leu Lys Lys Leu Gln Ile Asp Ile Arg Asp Ser Leu Ser Glu
312          370          375          380
314 Glu Glu Lys Glu Leu Leu Asn Arg Ile Gln Val Asp Ser Ser Asn Pro
315 385          390          395          400
317 Leu Ser Glu Lys Glu Lys Glu Phe Leu Lys Lys Leu Lys Leu Asp Ile
318          405          410          415
320 Gln Pro Tyr Asp Ile Asn Gln Arg Leu Gln Asp Thr Gly Gly Leu Ile
321          420          425          430
323 Asp Ser Pro Ser Ile Asn Leu Asp Val Arg Lys Gln Tyr Lys Arg Asp
324          435          440          445
326 Ile Gln Asn Ile Asp Ala Leu Leu His Gln Ser Ile Gly Ser Thr Leu
327          450          455          460
329 Tyr Asn Lys Ile Tyr Leu Tyr Glu Asn Met Asn Ile Asn Asn Leu Thr
330 465          470          475          480
332 Ala Thr Leu Gly Ala Asp Leu Val Asp Ser Thr Asp Asn Thr Lys Ile
333          485          490          495

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VERIFICATION SUMMARY

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